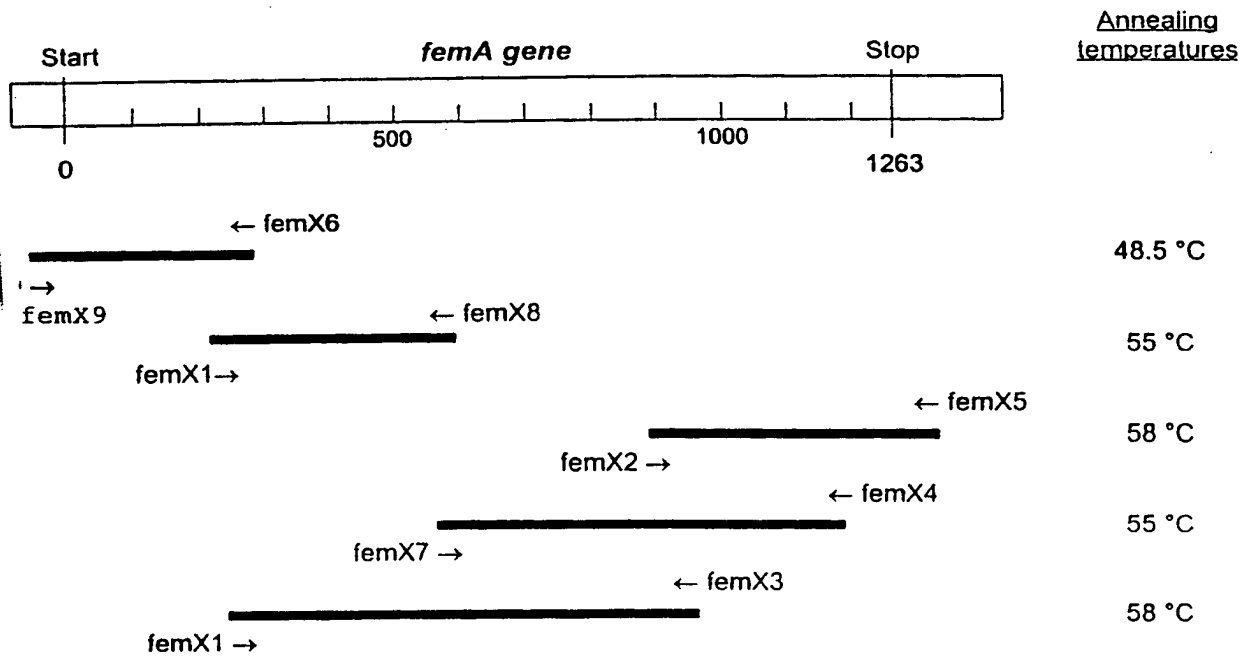


1/20

Oligonucleotides

femX1	TTCMAATCGCGGTCCAGT	213-230
femX2	CAAGAACATGGCAACGAATTACC	913-935
femX3	TGGGTAATTCGTTGCCATGTTCT	937-915
femX4	CCAAGCATCTTCAGCATCTTC	1133-1113
femX5	TTCTTTAACTGTAACTCTGTAAATTTCA	1309-1281
femX6	ACATATTTACTTAATTCGTTAAAGAA	290-265
femX7	CAGAAAAATGGTGTTAAAGTAAGATTT	559-585
femX8	AAGAAATCTTACTT TCACACCATTTT	588-562
femX9	AACTCGAAAATAGAACTA	(-43)-(-26)

FIG. 1

FIG2a

S. haemolyticus	gag-t-----g-----a-----a-a-t-c-g-g-tg-caat-a---a-taag--c-at-t-t-----c-a--a-tgact-aa
S. hominis	aggaggtata gag-t-----g-----a-----a-a-t-c-g-g-tg-cgat-t---t-aaaa--c-at-t-c-----t-a--g-tgact-aa
S. aureus	aataggagta atg-t-----g-----a-----a-a-t-a-g-g-tg-tgcc-t---a-tagc--c-at-c-t-----c-g--a-ctggt-gc
S. epidermidis	gggaggtatg aag-t-----g-----g-----g-a-t-a-a-ta-tgac-t---t-tcgt--a-at-t--a-tgga-gt
S. saprophyticus	aggaggtatat aaa-a-----a-----g-----a-t-a-a-g-g-cg-tgca-t---g-taaa--c-ga-t-t-----t-g--a-tgggt-ga
CONSENSUS	---A-AATGA A-TTTTAC-AA TTT-AC-GC- A-AGA-TT- G---T-TAC -GA-----ATG -C-A-A-AG-C ATTT-AC-CA -A-----G--100
S. haemolyticus	a-c-t-t-ga-g-ag---aa-taaaca--aa-t-ct-----t-t-t--a-a-t-a-g-----t-g--t-----a--c-ca-gt-g--a-a-a-a-
S. hominis	a-t-t-gt-a-ag---tg-gaaact--aa-tt-----a-a--t-a-t-a-g-----t-a--c-----t--t-ta-gc-a--t-t-t-a-
S. aureus	c-c-t-t-gt-a-gc---tg-aggtact--aa-a-tt-----g-a--a-a-c-t-a-----c-g--c-----a--t-ct-act--t-t-a-
S. epidermidis	a-t-c-at-a-gg---tg-aggtacc--gt-a-tt-----t-a--t-a-t-t-g-----c-a--g-----a--t-tt-at-a--a-t-t-
S. saprophyticus	a-t-t-at-g-aa---ag-aagtaca--aa-a-cc-----a-a-t--t-g-t-t-g-----t-a--a-----a--a-tt-act--a-t-t-
CONSENSUS	-A-TA-GA--T-AA--TTGC--A-----GA--C-CA--TAGT-GG-AT-AA-AA-AA--ATAA-GA-G-T-ATGC-GC-TG--T-T-AC-GC-GT-C200
S. haemolyticus	-a-c-----t-t-t-t-g--c-----t-cc-a--a-t-a-t--a-a-g-t--tag--g--t-t--c-tt-----t--g--aaca--
S. hominis	-c-t-----a-t-t-a--t-----a-tc-t--t-a-c-t-----a-g-a--caa--a--c-t--c-tt-----c--a-aagt--
S. aureus	-t-t-----g-g-c-g--t-----a-tc-c--t-a-g-t--a-g-a--tca--a--c-a-c-tt-----t--a-atca--
S. epidermidis	-t-a-----a-a-t-a--t-----c-tc-c--t-a-a-a--a-a-a--taa--g--t-a-t-tt-----t--a-gagt--
S. saprophyticus	-t-t-----t-c-c-g--t-----c-ta-a--t-a-a-c-a--t-t-g-a--taa--a--c-a-t-ac-----c--a-agca--
CONSENSUS	C-GT-ATGAA A-T-TT-AA-TA-TTTTATT C-AA-G-GG-CC-GT-AT-GATT-T-A-A-A--AGA-CT-GT-CA-T--TTCTTTAA-G A-TT-----AA300
S. haemolyticus	g--t-a---c-gc-taa-t gtc-----tg--tcgg-t-c--t-tt-ac-a-----t-ta-----t-t-t-aa--taca-gt--t-t-ta-t
S. hominis	a--t-a---c-ac-aca-t gtc-----tg--acgta-a-c--t-tt-gc-t-----tcgt-----t-t-t-ta--taca-ga--t-t-ga-t
S. aureus	a--g-t---a-ac-tcg-t gtc-----cc-acata-c--t--tt-ac-a-----acata-c--t--a-tt-ac-a-----ctg-----t-c-ga
S. epidermidis	a--g-a---a-at-taa-t gtc-----tt-aaggt-c--a-cc-tc-a-----t-ta-----t-ta-----g-a-aa--aact-ga--a-tc-t
S. saprophyticus	a--g-a---a-ac-taa-g cct-----tt-acgg-a-t--t-tc-tg-t-----tcgt-----t-t-t-ag--atta-ca--g-tc-c
CONSENSUS	-TAT-TAAA-A-A-A--T-----TATA-T-----T-GA-CC-TA-T--C-TATCAATA-----AATCAT GA-GG-GA--T-----G-AA TGC-GG--A-400
S. haemolyticus	-----t-c--t--a-ga-gaagcatc-c--a-t-g-a--tgaa--c-----tact-aa-t-----t-ga--taaa-----cc-a-at-t--t-tt-g
S. hominis	-----t-c--c---a-aa-gaacaat-a--a-c-a--cgaa--g-----taca-ca-a-----t-t-aa--atta-----tc-g-tc-t--a-tt-a
S. aureus	-----t-c--t--a-aa-gagtaact-a--a-t-g-a--tact--a-----ccat-aa-a-----t-tg--gcta-----tc-t-at-c--a-gt-g
S. epidermidis	-----a-t--t--g-at-agagagt-t-a-a-a-a--cgaa--a-----ccac-aa-a-----t-tg--atta-----cc-a-at-t--t-tc-a
S. saprophyticus	-----a-t--t--a-aa-gaaacaac-c--t-a-a-g--tgaa--t-----ttta-ct-c-----c-aa--actt-----aa-a-tc-t--t-tt-g
CONSENSUS	GATTGG-T-T-T-GAT-A-T-----T-----GG-T-T-A-C-A-----CG-TT-----A-GG-TTGA-CC--T-----CAAAAT--G-T-CA-TC-GT-TA-500
S. haemolyticus	-----aaaaa t-----cat-t a-a-ta-at-a--tgga-----a-tc-a c-t-ac-t--t-t-----tc-a-a--t-g-----taag--
S. hominis	-----aagga t-----ctg-t a-a-tg-at-a--tgga-----a-tt-a c-a-aa-a--t-t-----cc-a-a--t-t-----aaga--
S. aureus	-----aagga t-----cag-a g-t-ca-ca--t-aaat-----g-ac-t a-a-aa-a--c-g-----ta-a-g--t-t-----aaga--
S. epidermidis	-----gcaaa c-----gtg-t a-a-tg-tt-a--aaac-----g-tt-a a-a-gc-t--t-t-----ta-g-a--t-a-----ccgc--
S. saprophyticus	-----gctgg a-----ctg-t a-a-cg-ac-t-tcgg-----a-tt-a c-t-ac-a--t-t-----ac-g-a--t-t-----aaga--
CONSENSUS	ATTTA-----AAAA--C--A-GA--T--T-AA-----AT GGAT-G-T--G-AA--G-A-A-AC-AAAAA ACT-A-AA-AATGG-GT-A AAGT-----TT600
S. haemolyticus	ct-atacag--a-a-ac-t-a--a-c-cc-t-----t-----a-----aa--c-aa-g--a-aa-ccaa--a-a-t--tagt--c--t-t-tc-c
S. hominis	tc-tacta--a-a-at-a--t-t-ca-a-----t-----a-----at--a-ga-t--a-aa-ttct--a-a-g--tagt--t--c-t-tc-a
S. aureus	tt-atctg--a-a-ac-a--a-t-ta-a-----t-----a-----gt--a-at-a--act-tgct--c-t-t--caaa--t--c-g-tc-c
S. epidermidis	tt-atctg--a-a-gt-a--t-a-ta-g-----t-----g-----ct--t-aa-t--a-at-tgca--a-a-a--tagt--t--t-c-ca-a
S. saprophyticus	tt-aggtg--t-t-gt-g--a-a-cc-c-----c-----a-----tt--t-aa-a--g-at-tgac--a-a-t--cgat--t--t-t-ta-g
CONSENSUS	--T-----AA GA-GA--T-C C-AT-TT--G TCAAT-ATG GA-GATAC--C-GA--C-AA--G--TT-----CAT-G-GA-G A-----TT-TA -TA-AA--G-700





SECRET

NNNNNNNN NNNAAATGA ANTTTACNAA TTTNACNGCN ANAGANTTNN GNNNTNTATC NGANNNTATG NCNNANAGNC ATTTNACNCA NANNNNNGNN  
NANTANGANN TNAANNTTGC NNAANNNNNN GANNCCANN TAGTNGGNAT NAANAANAAN NATANGANG TNATTGCNGC NTGNTNTNTN ACNGCNGTNC  
CNGTATGAA ANTNTTNAAN TANTTTTATT CNAANNNGG NCCNGTNAATN GATTNTNANA ANNNAGANCT NGTNCANTNN TTCTTTAANG ANTNNNNAA  
NTATNTNAAA NANNANNNTN NNNTATANT NNNTNTNGAN CCNTANNNTN CNTATCAATA NNNNAATCAT GANGGANGNN TNNNGNNA TGCNGGNNAN  
GATTGGTNT TNGATNANNT NNNNNNNNTN GGNTNTNANC ANNNNGGNTT NNNNANGGN TTTGANCNN TNNNCAAAT NNGTNNCAN TCNGTNTNTAN  
ATTTANNNN NAAANNNCN NANGANNNTN TNAANNNTN GGATNGNNTN NGNAANNNGNA ANACNAAAA AGTNANAAN AATGGNGTNA AAGTNNNTT  
NNTNNNNNAA GANGANNNTC CNATNTTNG NTCATTNATG GANGATACNN CNGANNCNAA NGNTTNNNN GATNGGANG ANNNNTNTA NTANAANNNGN  
TNNNNNNTT NNAAGANN NGTNTNGTN CCNTNGCNT ATATNNNTT TGATGANTAN NTNNNGAAN TNNANNNGA NNGNNNNNN NTNANTAAAG  
ANNNAANA AGCNTNAAN GANATNGANA AANGNCCNGA NAANAAAAAN GCNNNNAANA ANNNNNNNAA NNTNNAAN CAANTNNNG CNAANNANCA  
AANNNTNAN GANGNNANN NNNTNNAAN NNANCATGGN AANGAATTAC CNATNTCNGC NGNTNCTTN NTNATNAATC CNTNTGAAGT NGTNTANTAN  
GCNGGTGGNA CNTCNAATNN NTNNNGCAN TTNGCNGGNA GNTATGCNNT NCAATGGNN ATGATTAAAT ATGCNNTNNA NCATNNNATN NANNGTANA  
ATTTNTATGG NNTAGNGGT NANTTTANNG ANGANGCNGA AGATGNGGN GTNTNAAAT TNAAAAAAGG NTNNNATGCN GANNNTNTNG ANTANGTTGG  
NGANTTNTN AAACCNATNA ANAANCNNT NTANNNNNN TATANNNCAN TNAAAAAANT NNAANNNNAN NNNNNNTANN NANNNNNNNA NNNNANNNN  
NNNNNATGA AATTACAG AGTTAANN

FIG. 3CONSENSUS SEQUENCE

220 bases	<i>S.aureus</i>	<i>S.epidermidis</i>	<i>S. hominis</i>
<i>S.aureus</i>	-	-	-
<i>S.epidermidis</i>	17.7	-	-
<i>S.hominis</i>	13.2	16.8	-
<i>S.saprophyticus</i>	17.3	18.6	16.8

Base % ( non appariated ) between the primers bioU1 and bioU3  
FIG4a

FIG. 4b

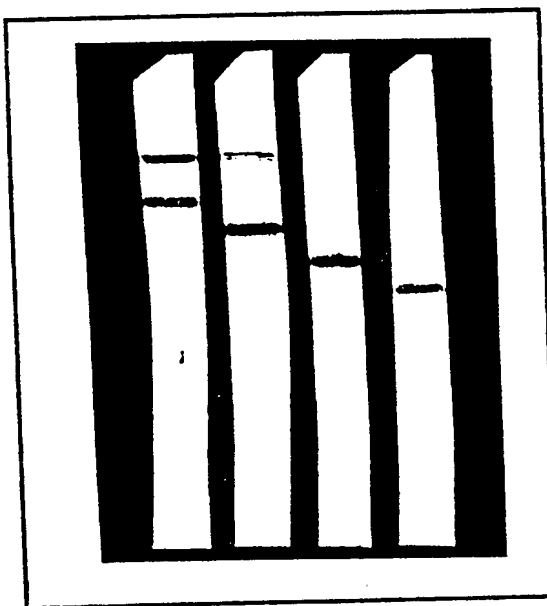
1 : mecA

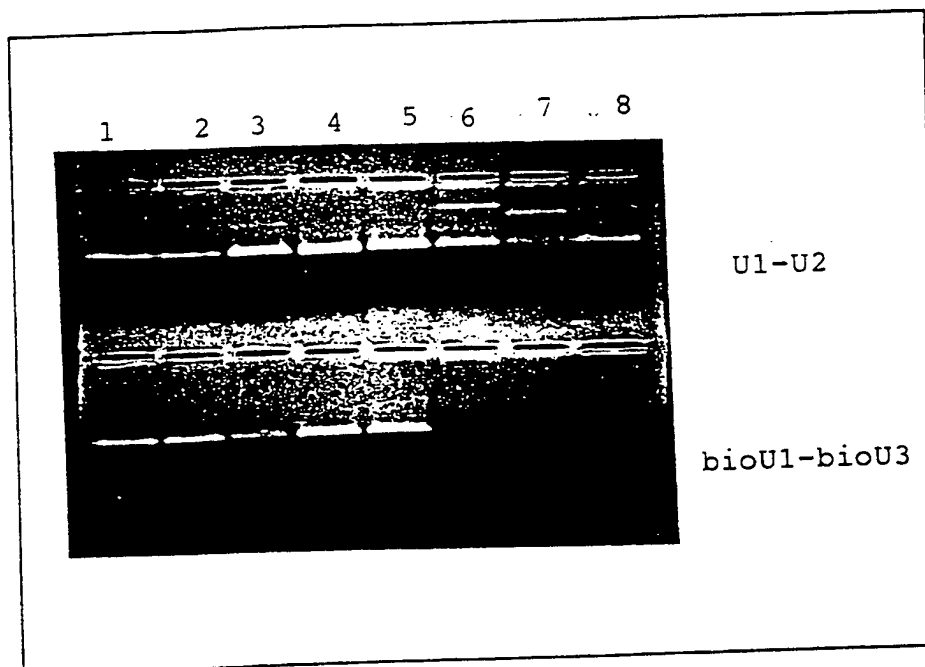
2: femA Sau

3. femA Sep

4. femA Sho

5. femA Ssa



FIG.5

AMPLIFICATION of CNS SPECIES under UNIVERSAL CONDITIONS.

- (1) : *S. haemolyticus*
- (2) : *S. capitis*
- (3) : *S. cohnii*
- (4) : *S. xylosus*
- (5) : *S. simulans*
- (6) : *S. lugdunensis*
- (7) : *S. schleiferi*
- (8) : *S. warneri*

Th(reaction PCR) = 48°C

.7/20  
S. haemolyticus FIG. 6a

10 30 50  
ATAATGAAGTTTACAAATTTAACAGCTACAGAGTTTGGCAATTATACAGATAAGATGCCA  
MetLysPheThrAsnLeuThrAlaThrGluPheGlyAsnTyrThrAspLysMetPro

70 90 110  
TATAGTCATTTACACAAATGACTGAAACTATGAGATGAAAGTTGCAAATAAACAGAA  
TyrSerHisPheThrGlnMetThrGluAsnTyrGluMetLysValAlaAsnLysThrGlu

130 150 170  
ACTCACTTAGTTGGTATAAAAAATAAGATAATGAGGTTATTGCAGCCTGCATGTTGACA  
ThrHisLeuValGlyIleLysAsnLysAspAsnGluValIleAlaAlaCysMetLeuThr

190 210 230  
GCAGTACCAGTCATGAAATTTTTTAAGTACTTTTATTCTAACCGAGGACCTGTAATTGAT  
AlaValProValMetLysPhePheLysTyrPheTyrSerAsnArgGlyProValIleAsp

250 270 290  
TATGATAATAGAGAGCTTGTTCACTTTTTCTTTAATGAGTTAACAAAGTATTTAAACAG  
TyrAspAsnArgGluLeuValHisPhePhePheAsnGluLeuThrLysTyrLeuLysGln

310 330 350  
CATAATTGTCTATATGTTTCGAGTTGACCCTTATTTACCATATCAATATTTAAATCATGAT  
HisAsnCysLeuTyrValArgValAspProTyrLeuProTyrGlnTyrLeuAsnHisAsp

370 390 410  
GGTGAAATTACAGGTAATGCTGGTAATGATTGGTTCTTTGATAAGATGAAGCATCTCGGA  
GlyGluIleThrGlyAsnAlaGlyAsnAspTrpPhePheAspLysMetLysHisLeuGly

430 450 470  
TTTGAACATGAAGGCTTTACTAAAGGTTTTGATCCGATTAAACAAATCCGATATCATTCT  
PheGluHisGluGlyPheThrLysGlyPheAspProIleLysGlnIleArgTyrHisSer

490 510 530  
GTTTTAGATTTAAAAAATAAAACATCTAAAGATATATTAAATGGAATGGATAGTCTACGT  
ValLeuAspLeuLysAsnLysThrSerLysAspIleLeuAsnGlyMetAspSerLeuArg

550 570 590  
AAACGTAATACTAAAAAAGTTCAAAAAATGGTGTGAAAGTTAAGTTCTTATCAGAAGAA  
LysArgAsnThrLysLysValGlnLysAsnGlyValLysValLysPheLeuSerGluGlu

610 630 650  
GAACTTCCAATCTTCCGTTTATTTATGGAAGATACAACCGAAACGAAAGAATTCCAAGAT  
GluLeuProIlePheArgSerPheMetGluAspThrThrGluThrLysGluPheGlnAsp

670 690 710  
AGAGATGATAGTTTCTATTATAATCGCTATAGACATTTCAAAGATCACGTGCTTGTACCA  
ArgAspAspSerPheTyrTyrAsnArgTyrArgHisPheLysAspHisValLeuValPro

8/20

770

CTAGCTTATATTAAGTTTGTATGAGTACATCGAAGAATTACAAAATGAACGTGAAACTTTA  
LeuAlaTyrIleLysPheAspGluTyrIleGluGluLeuGlnAsnGluArgGluThrLeu

730

750

790

810

830

AATAAAGATGTTAATAAAGCTTTAAAAGATATTGAAAAACGACCAGACAATAAAAAGGCA  
AsnLysAspValAsnLysAlaLeuLysAspIleGluLysArgProAspAsnLysLysAla

850

870

890

TTTAATAAAAAAGAAAATCTTGAAAAACAATTAGATGCCAATCAACAAAAATTAGACGAG  
PheAsnLysLysGluAsnLeuGluLysGlnLeuAspAlaAsnGlnGlnLysLeuAspGlu

910

930

950

GCTAAAAAATTACAAGCCGAACATGGTAATGAATTACCAATTTTCAGCAGGTTTCTTCTTT  
AlaLysLysLeuGlnAlaGluHisGlyAsnGluLeuProIleSerAlaGlyPhePhePhe

970

990

1010

ATTAATCCATTTGAAGTTGTTTATTATGCAGGTGGAACCTTCTAATAAATATAGACATTTT  
IleAsnProPheGluValValTyrTyrAlaGlyGlyThrSerAsnLysTyrArgHisPhe

1030

1050

1070

GCAGGCAGTTATGCTATTCAATGGACAATGATTAAGTATGCAATTGATCATGGTATTGAT  
AlaGlySerTyrAlaIleGlnTrpThrMetIleAsnTyrAlaIleAspHisGlyIleAsp

1090

1110

1130

AGATACAATTTCTATGGTATTAGCGGTAATTTTAGTGAAGACGCTGAAGATGTTGGAGTC  
ArgTyrAsnPheTyrGlyIleSerGlyAsnPheSerGluAspAlaGluAspValGlyVal

1150

1170

1190

ATTAAATTTAAAAAGGTTTCAATGCAGACGTAATTGAGTATGTTGGAGACTTTGTGAAA  
IleLysPheLysLysGlyPheAsnAlaAspValIleGluTyrValGlyAspPheValLys

1210

1230

1250

CCTATTAACAAACCTTTGTATTCAAGTGTATAAGACACTCAAAAAGATTAAAAAAGATTT  
ProIleAsnLysProLeuTyrSerValTyrLysThrLeuLysLysIleLysLysArgPhe

1270

1290

AATTAAAGAGGGGAATAGACGAATATGAAATTTACAGAGTTAAAC  
AsnEndArgGlyGluEndThrAsnMetLysPheThrGluLeuAsn

FIG. 6b

S. lugdunensisFIG. 7a

10 30 50  
ACAGCAAATGAATTCGGTGATTTTCACAGATCAAATGCCATATAGTCATTTTACTCAAATG  
ThrAlaAsnGluPheGlyAspPheThrAspGlnMetProTyrSerHisPheThrGlnMet

70 90 110  
ACAGGTAAGTATAATTTAAAGTTGCCGAAAAACAGAAACACATTTAGTTGGTGTAA  
ThrGlyAsnTyrAsnLeuLysValAlaGluLysThrGluThrHisLeuValGlyValLys

130 150 170  
AATAATAATAACGAAGTAATTGCAGCATGTTTATTGACAGCTGTACCAGTCATGAAGTTT  
AsnAsnAsnAsnGluValIleAlaAlaCysLeuLeuThrAlaValProValMetLysPhe

190 210 230  
TTTAAATACTTTTACAGCAATAGAGGCCAGTTATAGATTATGCTAACCAAGAACTTGTA  
PheLysTyrPheTyrSerAsnArgGlyProValIleAspTyrAlaAsnGlnGluLeuVal

250 270 290  
CATTTTTCTTTAATGAGCTAACTAAATATTTAAAAAAGTATAACTGTCTCTATGTCCGC  
HisPhePhePheAsnGluLeuThrLysTyrLeuLysLysTyrAsnCysLeuTyrValArg

310 330 350  
ATAGATCCATACTTACCTTATCAATATAGAGACCATGACGGTAATATAACGGCAAATGCT  
IleAspProTyrLeuProTyrGlnTyrArgAspHisAspGlyAsnIleThrAlaAsnAla

370 390 410  
GGCAATGATTGGTTTTTCAATAAAATGGAACAACCTCGGATACCATCATGATGGCTTTACA  
GlyAsnAspTrpPhePheAsnLysMetGluGlnLeuGlyTyrHisHisAspGlyPheThr

430 450 470  
ACAGGATTTGATCCAATATTACAAATCAGATTCCATTCTATTCTTAATTTAAAGGATAAG  
ThrGlyPheAspProIleLeuGlnIleArgPheHisSerIleLeuAsnLeuLysAspLys

490 510 530  
ACAGCTAAAGATGTTTTAAATAATATGGATAGTTTACGTAAAAGAAATACCAAAAAAAGT  
ThrAlaLysAspValLeuAsnAsnMetAspSerLeuArgLysArgAsnThrLysLysSer

550 570 590  
TCAAAAAATGGAGTCAAAGTAAAGTTCCTTACTGAAGAAGAACTACCTATCTTTTCGTTCA  
SerLysAsnGlyValLysValLysPheLeuThrGluGluGluLeuProIlePheArgSer

610 630 650  
TTTATGGAGCAGACGTCAGAATCTAAAGAATTCTCTGATAGAGACGACCAATTTTATTAC  
PheMetGluGlnThrSerGluSerLysGluPheSerAspArgAspAspGlnPheTyrTyr

670 690 710  
AATCGGTTTAAAGTACTATAAAGATAGGGTGCTTGTGCCTCTAGCATATTTAAATTTGAT  
AsnArgPheLysTyrTyrLysAspArgValLeuValProLeuAlaTyrLeuLysPheAsp

730 750 770  
GAATATATAGAAGAACTAACGAATGAACGACAACTTTAGAAAAAGATTTAGGCAAAGCA  
GluTyrIleGluGluLeuThrAsnGluArgGlnThrLeuGluLysAspLeuGlyLysAla

790 810 830  
CTTAAAGACATTGAGAAACGACCAGATAACAAAAAGCTTATAATAAACGAGACAACCTA  
LeuLysAspIleGluLysArgProAspAsnLysLysAlaTyrAsnLysArgAspAsnLeu

850 870 890  
CAACAACAACTCGATGCCAATCAACAAAAGTTAAATGAGGCTAATCAGTTACAAGCGGAA  
GlnGlnGlnLeuAspAlaAsnGlnGlnLysLeuAsnGluAlaAsnGlnLeuGlnAlaGlu

910 930 950  
CACGGTAATGAGTTACCTATCTCTGCCGGTTTCTTTATTATTAAATCCGTTTGAAGTTGTA  
HisGlyAsnGluLeuProIleSerAlaGlyPhePheIleIleAsnProPheGluValVal

970 990 1010  
TACTACGCTGGAGGTACCGCTAATAAATATCGTCATTTTGCAGGTAGTTACGCGGTTTCAG  
TyrTyrAlaGlyGlyThrAlaAsnLysTyrArgHisPheAlaGlySerTyrAlaValGln

1030 1050 1070  
TGGACTATGATTAACCTATGCTATCGAACACGGCATAGACAGATATAATTTCTACGGCATT  
TrpThrMetIleAsnTyrAlaIleGluHisGlyIleAspArgTyrAsnPheTyrGlyIle

1090 1110 1130  
AGTGGAACTTCTCAGATGATGCTGAAGACGCAGGTGTCATTTCGCTTTAAAAAAGGTTAT  
SerGlyAsnPheSerAspAlaGluAspAlaGlyValIleArgPheLysLysGlyTyr

1150 1170 1190  
GGTGCAGAAGTGATTGAATACGTTGGTGATTTTGTAAAACCTATAAATAAACCTATGTAT  
GlyAlaGluValIleGluTyrValGlyAspPheValLysProIleAsnLysProMetTyr

1210 1230 1250  
AAACTTTATTTCAGTGTTAAAACGAATTCAAAATAAGCTATAGAGGAGAATGGATTAATTA  
LysLeuTyrSerValLeuLysArgIleGlnAsnLysLeuEndArgArgMetAspEndLeu

1270  
TGAAATTTACAGAGTTTAAC  
EndAsnLeuGlnSerLeu

FIG. 7b

11/20  
S. xylosus

FIG. 8a

10 30 50  
ACGCAAAAGAGTTTGGGTGCATTTTCAGATAAAAATGCCAAATAGCCATTTTCACGCAAATG  
ThrGlnLysSerLeuGlyAlaPheSerAspLysMetProAsnSerHisPheThrGlnMet

70 90 110  
GTAGGGAATTATGAATTGAAAATTGCAGAAAGTACTGAAACACATTTAGTAGGTATAAAA  
ValGlyAsnTyrGluLeuLysIleAlaGluSerThrGluThrHisLeuValGlyIleLys

130 150 170  
AACAAATGATAATGAAGTCATTGCAGCTTGTATTATTAAGTGCAGTACCAGTAATGAAATTC  
AsnAsnAspAsnGluValIleAlaAlaCysLeuLeuThrAlaValProValMetLysPhe

190 210 230  
TTTAAGTATTTTTATACTAATAGAGGTCCGGTTATAGATTTTGAAAATAAAGAATTAGTG  
PheLysTyrPheTyrThrAsnArgGlyProValIleAspPheGluAsnLysGluLeuVal

250 270 290  
CATTACTTTTTCAATGAACCTATCTAAATATGTGAAAAACATAATGCGCTTTATTTAAGA  
HisTyrPhePheAsnGluLeuSerLysTyrValLysLysHisAsnAlaLeuTyrLeuArg

310 330 350  
GTTGATCCTTATTTAGCATATCAATACCGTAATCATGATGGTGAGGTATTGGAAAATGCA  
ValAspProTyrLeuAlaTyrGlnTyrArgAsnHisAspGlyGluValLeuGluAsnAla

370 390 410  
GGACATGATTGGATTTTCGATAAAATGAAGCAGCTTGGATATAAACACCAAGGATTTTTA  
GlyHisAspTrpIlePheAspLysMetLysGlnLeuGlyTyrLysHisGlnGlyPheLeu

430 450 470  
ACTGGTTTCGATTCAATTATTCAAATTAGGTTCCACTCTGTACTGGATTTAGTAGGTAAA  
ThrGlyPheAspSerIleIleGlnIleArgPheHisSerValLeuAspLeuValGlyLys

490 510 530  
ACTGCTAAAGATGTACTAAATGGTATGGATAGTTTACGTAAACGTAATACTAAAAAAGTA  
ThrAlaLysAspValLeuAsnGlyMetAspSerLeuArgLysArgAsnThrLysLysVal

550 570 590  
CAAAAAAATGGCGTGAAAGTAAGGTTCTTAAGGGAAGATGAGTTGCCAATTTTCCGTTCA  
GlnLysAsnGlyValLysValArgPheLeuArgGluAspGluLeuProIlePheArgSer

610 630 650  
TTCATGGAAGATACATCTGAACTAAAGACTTTGACGATAGAGACGATGGCTTTTACTAC  
PheMetGluAspThrSerGluThrLysAspPheAspAspArgAspAspGlyPheTyrTyr

670 690 710  
AATAGATTAAGGTATTATAAAGATCGCGTATTAGTACCTCTAGCTTATATGGATTTCAAT  
AsnArgLeuArgTyrTyrLysAspArgValLeuValProLeuAlaTyrMetAspPheAsn

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730 750 770  
GAATATATTGAAGAATTGCAAGCTGAACGTGAGGTGTTAAGCAAAGATATCAATAAAGCA  
GluTyrIleGluGluLeuGlnAlaGluArgGluValLeuSerLysAspIleAsnLysAla

790 810 830  
GTAAAAGATATCGAGAAAAGACCTGAAAATAAAAAAGCATATAATAAAAAAGATAATCTA  
ValLysAspIleGluLysArgProGluAsnLysLysAlaTyrAsnLysLysAspAsnLeu

850 870 890  
GAGAAACAACCTTATAGCGAATCAACAAAAAATTGATGAAGCTAAAACCTCTACAAGAGAAG  
GluLysGlnLeuIleAlaAsnGlnGlnLysIleAspGluAlaLysThrLeuGlnGluLys

910 930 950  
CATGGTAACGAACTACCAATCTCAGCAGCATATTTTCATCATTAAACCCTTATGAAGTAGTG  
HisGlyAsnGluLeuProIleSerAlaAlaTyrPheIleIleAsnProTyrGluValVal

970 990 1010  
TATTATGCGGGTGAACGTCAAATGAGTTTAGACATTTTGCTGGTAGTTATGCCATTCAA  
TyrTyrAlaGlyGlyThrSerAsnGluPheArgHisPheAlaGlySerTyrAlaIleGln

1030 1050 1070  
TGGAAGATGATTAACCTATGCTATTGACCATAATATTGATAGATATAATTTTTATGGAATT  
TrpLysMetIleAsnTyrAlaIleAspHisAsnIleAspArgTyrAsnPheTyrGlyIle

1090 1110 1130  
AGTGGTCATTTTACAGAAGATGCAGAAGATGCCGGTGTAGTTAAATTTAAAAAAGGATTT  
SerGlyHisPheThrGluAspAlaGluAspAlaGlyValValLysPheLysLysGlyPhe

1150 1170 1190  
AATGCGGATGTAGTGGAATATGTTGGTGATTTTATTAAACCAATCAATAAACCAATGTAC  
AsnAlaAspValValGluTyrValGlyAspPheIleLysProIleAsnLysProMetTyr

1210 1230 1250  
AAAATTTATACGACATTAAAGAAAATTAAAGATAAAAAAGAAATAAACATTTAATAGAAGG  
LysIleTyrThrThrLeuLysLysIleLysAspLysLysLysEndThrPheAsnArgArg

1270 1290  
GAACTAAGCTAGAATGAAATTTACAGAGTTAAACC  
GluLeuSerEndAsnGluIleTyrArgValLys

FIG. 8b

S. capitisFIG. 9a

10 30 50  
ACAGCTAAAGAATTTAGTGA CTTTACTGATCAAATGCCTTATAGCCATTTTACTCAGATG  
ThrAlaLysGluPheSerAspPheThrAspGlnMetProTyrSerHisPheThrGlnMet

70 90 110  
GAAGGTAATTATGAACTTAAAGTTGCTGAAGGTACGGATTACATCTCGTAGGAATTAAA  
GluGlyAsnTyrGluLeuLysValAlaGluGlyThrAspSerHisLeuValGlyIleLys

130 150 170  
AATAATGACAACCAAGTGATTGCAGCATGTTTATTAAGTGTACCTGTAATGAAAATT  
AsnAsnAspAsnGlnValIleAlaAlaCysLeuLeuThrAlaValProValMetLysIle

190 210 230  
TTTAAATATTTTTACTCAAATCGCGGGCCAGTGATTGATTATGATAATAAGAGCTTGTT  
PheLysTyrPheTyrSerAsnArgGlyProValIleAspTyrAspAsnLysGluLeuVal

250 270 290  
CACTTTTTCTTTAATGAATTAAGTAAATATGTAAAAAGCATAATTGTCTTTATCTAAGA  
HisPhePhePheAsnGluLeuSerLysTyrValLysLysHisAsnCysLeuTyrLeuArg

310 330 350  
GTTGACCCCTTATCTTCCTTATCAATACTTAAATCATGACGGTGAAATTATTGGAAATGCT  
ValAspProTyrLeuProTyrGlnTyrLeuAsnHisAspGlyGluIleIleGlyAsnAla

370 390 410  
GGCCATGATTGGTTTTTCAATAAGATGGAAGAATTAGGATTTGAACATGAAGGCTTTTCAT  
GlyHisAspTrpPhePheAsnLysMetGluGluLeuGlyPheGluHisGluGlyPheHis

430 450 470  
AAAGGCTTCCATCCTATCTTACAAGTAAGATATCATTTCAGTTTTAGATTTAAAAGATAAA  
LysGlyPheHisProIleLeuGlnValArgTyrHisSerValLeuAspLeuLysAspLys

490 510 530  
ACGGCTAAAGATGTACTCAAAGGAATGGATAGTTTAAAGAAAGCGTAATACTAAGAAAGTA  
ThrAlaLysAspValLeuLysGlyMetAspSerLeuArgLysArgAsnThrLysLysVal

550 570 590  
CAAAAAAATGGTGTCAAAGTCCGTTTCCTATCCGAAGATGAATTACCTATCTTTAGATCA  
GlnLysAsnGlyValLysValArgPheLeuSerGluAspGluLeuProIlePheArgSer

610 630 650  
TTTATGGAAGATACTACAGAAACGAAAGAGTTTCGCCGATAGAGATGATAGTTTCTATTAT  
PheMetGluAspThrThrGluThrLysGluPheAlaAspArgAspAspSerPheTyrTyr

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670 690 710  
AATCGATTAAATACTTTAAAGATAGAGTATTAGTACCATTAGCATATGTTGACTTCGAT  
AsnArgLeuLysTyrPheLysAspArgValLeuValProLeuAlaTyrValAspPheAsp

730 750 770  
GAGTATATTGAAGAACTTAATAATGAAAGAGATGTTCTTAATAAAGATTTAAATAAGGCG  
GluTyrIleGluGluLeuAsnAsnGluArgAspValLeuAsnLysAspLeuAsnLysAla

790 810 830  
CTCAAAGATATTGAGAAGAGACCTGATAATAAGAAAGCTTATAACAAAAGAGATAATCTT  
LeuLysAspIleGluLysArgProAspAsnLysLysAlaTyrAsnLysArgAspAsnLeu

850 870 890  
CAACAACAATTAGATGCAAATCAACAAAAAATTGATGAAGCTAAAACTTACAACAAGAA  
GlnGlnGlnLeuAspAlaAsnGlnGlnLysIleAspGluAlaLysAsnLeuGlnGlnGlu

910 930 950  
CATGGTAATGAATTACCTATTTTCAGCTGGATATTTCTTCATTAATCCGTTTGAAGTTGTT  
HisGlyAsnGluLeuProIleSerAlaGlyTyrPhePheIleAsnProPheGluValVal

970 990 1010  
TATTACGCAGGTGGCACATCGAATCGTTATCGTCACTATGCCGGAAGTTATGCAATTCAA  
TyrTyrAlaGlyGlyThrSerAsnArgTyrArgHisTyrAlaGlySerTyrAlaIleGln

1030 1050 1070  
TGGAAAATGATAAACTATGCTTTAGAACATGGAATTAACCGTTATAATTTTTATGGAGTT  
TrpLysMetIleAsnTyrAlaLeuGluHisGlyIleAsnArgTyrAsnPheTyrGlyVal

1090 1110 1130  
AGTGGGGACTTCAGTGAAGACGCTGAAGATGTAGGAGTAATTAAGTTCAAAAAAGGCTAT  
SerGlyAspPheSerGluAspAlaGluAspValGlyValIleLysPheLysLysGlyTyr

1150 1170 1190  
AATGCTGATGTTATTGAATATGTAGGTGATTTTATCAAGCCAATCAATAAACCTATGTAT  
AsnAlaAspValIleGluTyrValGlyAspPheIleLysProIleAsnLysProMetTyr

1210 1230 1250  
GCAATCTATAACGCACTTAAAAAGTTAAAGAAATAGATTTTTTTTACCAACCCAATTATCT  
AlaIleTyrAsnAlaLeuLysLysLeuLysLysEndIlePheLeuProThrGlnLeuSer

1270  
AATTATGAAATTTACAGAGTTAA  
AsnTyrGluIleTyrArgVal

FIG. 9b

FIG. 10a  
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10 30 50  
ACGACGGCTGAATTTGGTGCCTTTACAGATCAAATGCCATATAGCCATTTCACGCAAATG  
ThrThrAlaGluPheGlyAlaPheThrAspGlnMetProTyrSerHisPheThrGlnMet

70 90 110  
GTAGGGAACTATGAATTAAAGGTTGCTGAAGGTGTTGAAACACATCTTGTCGGCATTAAA  
ValGlyAsnTyrGluLeuLysValAlaGluGlyValGluThrHisLeuValGlyIleLys

130 150 170  
GATAACAACAATAACGTACTAGCAGCATGTTTACTGACAGCAGTGCCAGTAATGAAGTTT  
AspAsnAsnAsnValLeuAlaAlaCysLeuLeuThrAlaValProValMetLysPhe

190 210 230  
TTTAAATATTTTTATTCAAACCGCGGACCAGTCTGGACTACGAAAATAAAGAGCTCGTT  
PheLysTyrPheTyrSerAsnArgGlyProValMetAspTyrGluAsnLysGluLeuVal

250 270 290  
CATTTCTTTTTTAATGAACTTTCAAATATGTTAAGAAATATCACGCATTGTATTGAGA  
HisPhePhePheAsnGluLeuSerLysTyrValLysLysTyrHisAlaLeuTyrLeuArg

310 330 350  
GTAGACCCTTATTTACCAATGTAAAGCGAAACCATGATGGTGAAGTGATTGAAAGATAC  
ValAspProTyrLeuProMetLeuLysArgAsnHisAspGlyGluValIleGluArgTyr

370 390 410  
GGCAGTGAAGTGGTTTTTTGATAAAATGGCTGAATTAACTTTGAACATGAAGGTTTCACA  
GlySerAspTrpPhePheAspLysMetAlaGluLeuAsnPheGluHisGluGlyPheThr

430 450 470  
ACTGGGTTTGATAACAATAAGGCAAATTCGTTTTTCATTCTGTGCTCGATGTTGAAAATAAA  
ThrGlyPheAspThrIleArgGlnIleArgPheHisSerValLeuAspValGluAsnLys

490 510 530  
ACATCAAAGACATCTTAAATCAAATGGATAATTTAAGGAAAAGAAATACGAAAAAAGTA  
ThrSerLysAspIleLeuAsnGlnMetAspAsnLeuArgLysArgAsnThrLysLysVal

550 570 590  
CAGAAAAATGGTGTGAAAGTCCGCTATCTAAACGAAGATGAATTACATATTTTCCGTTTCG  
GlnLysAsnGlyValLysValArgTyrLeuAsnGluAspGluLeuHisIlePheArgSer

610 630 650  
TTTATGGAAGATACATCTGAAACAAAAGATTTTGTAGATAGAGATGACGATTTTATTAT  
PheMetGluAspThrSerGluThrLysAspPheValAspArgAspAspPheTyrTyr

670 690 710  
CATCGTATGAAATACTATAAAGATCGTGTCCGCTACCACTAGCGTATATTGATTTTAAT  
HisArgMetLysTyrTyrLysAspArgValArgValProLeuAlaTyrIleAspPheAsn

730 750 770  
GCATATTTAGCAGAGCTCAACACTGAAGCGCAAGACTTTAAAAAAGAAATTGCAAAAGCA  
AlaTyrLeuAlaGluLeuAsnThrGluAlaGlnAspPheLysLysGluIleAlaLysAla

790 810 830  
GATAAAGACATCGACAAGCGTCCTGAAAATCAGAAAGCCATAAATAAAAAGAAAAATTTA  
AspLysAspIleAspLysArgProGluAsnGlnLysAlaIleAsnLysLysLysAsnLeu

850 870 890  
GAGCAACAACTAGAAGCGAATCAAGCTAAAATAAAGAAGCAGAAACATTGCAACTTAA  
GluGlnGlnLeuGluAlaAsnGlnAlaLysIleLysGluAlaGluThrLeuGlnLeuLys

910 930 950  
CACGGTGACACATTACCGATTTTCGGCTGGATTCTTTATTATTAATCCATTTGAGGTTGTT  
HisGlyAspThrLeuProIleSerAlaGlyPhePheIleIleAsnProPheGluValVal

970 990 1010  
TATTATGCAGGCGGCACAGCAAACGAATTTTCGTCATTTTGCTGGAAGCTACGCAGTGCAA  
TyrTyrAlaGlyGlyThrAlaAsnGluPheArgHisPheAlaGlySerTyrAlaValGln

1030 1050 1070  
TGCGAAATGATTAATTATGCGATTGATTATCAAATTCAGATATAACTTTTATGGCATT  
TrpGluMetIleAsnTyrAlaIleAspTyrGlnIleProArgTyrAsnPheTyrGlyIle

1090 1110 1130  
AGTGGTGATTTTTTCAGAAGATGCAGAAGATGCAGGTGTGATAAAATTTAAAAAAGGCTAT  
SerGlyAspPheSerGluAspAlaGluAspAlaGlyValIleLysPheLysLysGlyTyr

1150 1170 1190  
AATGCAGAAGTAATAGAATATGTCGGTGATTTTATTAAGCCTATAAACAAACCTGCCTAT  
AsnAlaGluValIleGluTyrValGlyAspPheIleLysProIleAsnLysProAlaTyr

1210 1230 1250  
ACAGTCTACTTAAAATTAAAGCAATTAAAGACAAGATAAAAAAGATAAGATATAGCAAAG  
ThrValTyrLeuLysLeuLysGlnLeuLysAspLysIleLysArgEndAspIleAlaLys

1270 1290  
AGAAGGGGATTTATTGGTATGAAATTTACAGAGTTAA  
ArgArgGlyPheIleGlyMetLysPheThrGluLeu

FIG.10b

S. sciuri 17/20FIG. 11a

10 30 50  
ACACTGGAATTTGAAGCTTTTACAAATAAAATGCCGTACGCGCATTTTACACAAGCAGTA  
ThrLeuGluPheGluAlaPheThrAsnLysMetProTyrAlaHisPheThrGlnAlaVal

70 90 110  
GGTAATTATGAATTA AAAACATCTGAAGGTACTTCAACACATTTAGTAGGGGTCAAAGAT  
GlyAsnTyrGluLeuLysThrSerGluGlyThrSerThrHisLeuValGlyValLysAsp

130 150 170  
AATCAAGGTGAAGTATTAGCTGCGTGTCTGTTAACAAGGTACCAGTTATGAAGAAATTT  
AsnGlnGlyGluValLeuAlaAlaCysLeuLeuThrSerValProValMetLysLysPhe

190 210 230  
AATTACTTTTACTCAAATAGAGGACCGTAATGGATTATGACAACAAAGAACTTGTTGAC  
AsnTyrPheTyrSerAsnArgGlyProValMetAspTyrAspAsnLysGluLeuValAsp

250 270 290  
TTTTTCTTTTAAAGAAATCGTGAGCTATTTAAAAAGTTATAAAGGATTATTCTTTAGAATC  
PhePhePheLysGluIleValSerTyrLeuLysSerTyrLysGlyLeuPhePheArgIle

310 330 350  
GATCCTTACTTGCCATATCAACTAAGAGATCATGATGGCAATATTAAAAAATCATTCAAC  
AspProTyrLeuProTyrGlnLeuArgAspHisAspGlyAsnIleLysLysSerPheAsn

370 390 410  
CGTGATGGTTTAATTAAACAATTTGAATCATTAGGTTATGAACACCAAGGCTTCACAAC  
ArgAspGlyLeuIleLysGlnPheGluSerLeuGlyTyrGluHisGlnGlyPheThrThr

430 450 470  
GGTTTCCACCCAATACATCAAATTAGATGGCATTCTGTACTTGATTAGAAAGTATGGAC  
GlyPheHisProIleHisGlnIleArgTrpHisSerValLeuAspLeuGluSerMetAsp

490 510 530  
GAAAAGACGCTCATCAAGAACATGGACAGTTTAAGAAAAAGAAATACTAAAAAAGTTCAA  
GluLysThrLeuIleLysAsnMetAspSerLeuArgLysArgAsnThrLysLysValGln

550 570 590  
AAAAATGGTGTTAAAGTTCGTTTTCTATCTAAAGATGAAATGCCGATATTCCGTCAATTT  
LysAsnGlyValLysValArgPheLeuSerLysAspGluMetProIlePheArgGlnPhe

610 630 650  
ATGGAAGATACTACAGAGAAGAAAGATTTCAACGATCGTGGCGATGACTTCTATTACAAT  
MetGluAspThrThrGluLysLysAspPheAsnAspArgGlyAspAspPheTyrTyrAsn

670 690 710  
AGATTAAAATACTTTGAAAATGTAAAGATTCTTTAGCATATATAGACTTTGAAACTTAC  
ArgLeuLysTyrPheGluAsnValLysIleProLeuAlaTyrIleAspPheGluThrTyr

730 750 770  
ATTCCACAATTAGAAAAAGAACATGAACAATACAACAAAGATATTGCAAAAGCTGAAAAA  
IleProGlnLeuGluLysGluHisGluGlnTyrAsnLysAspIleAlaLysAlaGluLys

790 810 830  
GATTTAGAAAAGAAACCAGATAATCAAAAAACGATTAATAAAATAGACAACCTTAAACAA  
AspLeuGluLysLysProAspAsnGlnLysThrIleAsnLysIleAspAsnLeuLysGln

850 870 890  
CAAAGAGAAGCAAATGAAGCTAAATTAGAAGAAGCACTTCAACTACAACAAGAACATGGT  
GlnArgGluAlaAsnGluAlaLysLeuGluGluAlaLeuGlnLeuGlnGlnGluHisGly

910 930 950  
GATACATTACCAATAGCAGCTGGTTTCTTTATTATTAAATCCATTTGAAGTTGTATATTAT  
AspThrLeuProIleAlaAlaGlyPhePheIleIleAsnProPheGluValValTyrTyr

970 990 1010  
GCAGGTGGTTTCATCGAATGAATATCGTCACCTTGCAGGTAGTTATGCAATTCAGTGGGAA  
AlaGlyGlySerSerAsnGluTyrArgHisPheAlaGlySerTyrAlaIleGlnTrpGlu

1030 1050 1070  
ATGATTAAATACGCGTTAGATCACAACATTGACCGTTATAACTTCTATGGTATCAGCGGA  
MetIleLysTyrAlaLeuAspHisAsnIleAspArgTyrAsnPheTyrGlyIleSerGly

1090 1110 1130  
GACTTCTCAGAAGATGCACCTGATGTTGGCGTTATTAAATTTAAAAAAGTTACAATGCA  
AspPheSerGluAspAlaProAspValGlyValIleLysPheLysLysGlyTyrAsnAla

1150 1170 1190  
GATGTTTATGAATATATTGGTGATTTTCGTTAAACCAATTAATAAACAGCGTACAAAGCA  
AspValTyrGluTyrIleGlyAspPheValLysProIleAsnLysProAlaTyrLysAla

1210 1230 1250  
TATACAACACTAAAAAAGTATTAATAAATAAATGATTTTCAGTAAGAGAGGAATTTAG  
TyrThrThrLeuLysLysValLeuLysLysEndMetIlePheSerLysArgGlyIleEnd

1270  
ATAATATGAAATTTACAGAGTTAA  
IleIleEndAsnLeuGlnSerEnd

FIG.11b

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100 taaaattttaaactcaactcaattctaaattctaaattaggagttatagagataatgaagttttacaaaattttacagactacagaaatttggcgcg  
M K F T N L T A T E F G D

200 ATTTTACTGAAAAAATGCCATATAGCCATTTTACACAGATGACTGAAATATTAGTGTAAAGTTGCTGAGAAAACTGAAACTCATTTAGTAGGAATTAA  
F T E K M P Y S H F T Q M T E N Y E L K V A E K T E T H L V G I K

300 AAATAAGATAATAAGATGCTGCTGTATGCTAACTGCTACCGTTATGAAAAATTTTAAATATTTTAAATCGTGGTCCAGTCAATTGAT  
N K D N E V I A A C M L T A V P V M K I F K Y F Y S N R G P V I D

400 TATGAAAAACAAGAACTCGTTCACTTTTCTTTAAAGAAATTAAGTAATATTAAAAACAACACATCTGTTTATATGCTAGTACGACCCCTTATTTGCCTT  
Y E N K E L V H F F F N E L S K Y L K Q Q H C L Y V R I D P Y L P Y

500 ATCAATATCGTAATCATGTGATATACAGGAAATGCTGGGAATGATGGTTCTTCGATAAAAAATGAAACAATTAGGATATCAACACGAAGGGTTTAC  
Q Y R N H D G D I T G N A G N D W F F D K M K Q L G Y Q H E G F T

600 AACAGGATTTGATCCAAATATTACAAATTCGGTTCATTCAGTTTTAAATTTAAAGGATAAACTGCTAAAGATGTATTAAATGGAATGGATAGTTTACGA  
T G F D P I L Q I R F H S V L N L K D K T A K D V L N G M D S L R

700 AAAAGAAATACTAAAAAGTCCAAAAAATGGTGTAAAGTAAGATTTCTTACTAAAGAAGAAATTACCTATTTTCAGATCATTTATGGAAGATACATCAG  
K R N T K K V Q K N G V K V R F L T K E E L P I F R S F M E D T S E

800 AGACTAAAGAATTTTCTGATAGAGGATAGTTTTTACTATAATCGATTTGATCATTTTAAAGATAGAGTATTAGTACCTCTCGCATATATAPAAAAATTTGA  
T K E F S D R E D S F Y Y N R F D H F K D R V L V P L A Y I K F D

900 TGAATATCTTGAAGAACTTCATGCAGAACGTCAGACATTAATAAAGACTTAAACAAGCTCTAAAGATATTGAAACAACGACGAGATACAAAAAGCA  
E Y L E E L H A E R Q T L N K D L N K A L K D I E K R P D N K K A

1000 CAAAATAAAAAAATAAATTAGAACAGCAATTAAGCAAAAAATTGTAAGCAACACAACTTCAATTTAGAACATGGTAAACGAATTACCAA  
Q N K K I N L E Q Q L K A N E Q K I D E A T Q L Q L E H G N E L P I

1100 TATCTGCTGGATCTTCTTTAATTAATCCATTTGAAGTTGTATATATGCAAGTGGAACTCAATAAATATAGACACTTCGTCGGAAGTTATGCAGTTCA  
S A G F F F I N P F E V V Y Y A G G T S N K Y R H F A G S Y A V Q

1200 ATGGACTATGATTAATATGCAATGATGCATGGCATGACCGTTATAATTTTATGGGATTAGTGGTCATTTTACAGATGATGCTGAAGATGCAGGTGT  
W T M I N Y A I D H G I D R Y N F Y G I S G H F T D D A E D A G V

1300 GTAAAAATTTAAAAAGGATTTAATGCAGATGTAATGAATATGTTGGTGATTTTCGTTAAACCTTATAAATAAACCAATGTATTCACTATATACAACACTTA  
V K F K K G F N A D V I E Y V G D F V K P I N K P M Y S L Y T T L K

AAAAATTTAAAAAGAGATTTGAATTAAGaggggaatagtgagaa 1343  
K I K K R L N ///

FIG.12

Staphylococcus saprophylticus

actgttagattagaactcgaaatagaactatagataaaggagatatataaaaaaTGAATTTACGAATTTAACTGCAAAAGAGTTCGGTG 100  
M K F T N L T A K E F G A  
CATTTACGGATAAAATGCCGAATAGTCATTTTCGCAATGGTTGGAAATTTATGAATTTGAATTTGCAAAAAGTACAGAAAACACACTAGTAGGTATTAA 200  
F T D K M P N S H F T Q M V G N Y E L K I A E S T E T H L V G I K  
GAATAATGATAATGAAGTAATTGCAGCATGTTTACTTACAGCTGTTCTCTGTATGAAATTTCTCAAGTATTTTATCCAAATAGAGGTCAGTCATAGAT 300  
N N D N E V I A A C L L T A V P V M K F F K Y F Y S N R G P V I D  
TTTGAATAAAGAACTCGTACATTACTTCTTAAACGAATTAGCAAAATATGTAAAAAACAATAATGCTTATATTTACGAGTAGATCCTTATCTTGCTT 400  
F E N K E L V H Y F F N E L A K Y V K K H N A L Y L R V D P Y L A Y  
ATCAATATCGTAATCATGATGGTGAAGTATTAGCAAAATGCGGTACGATTGGAATTTTGTGATAAAATGAACAACACTCGGTTATAAGCATGAAGGTTTTTT 500  
Q Y R N H D G E V L A N A G H D W I F D K M K Q L G Y K H E G F L  
AACTGGCTTTGACCCAATACTTCAAAATAGATTCATTTCTGTTTAGATTTTAGCTGGAAAACACTGCTAAAGACGTACTTAATGGTATGGATGTTTACGT 600  
T G F D P I L Q I R F H S V L D L A G K T A K D V L N G M D S L R  
AAACGAATATAAAGTACAGAAAATGGTGTGAAGTAAGATTTTATAGTGAAGATGAGTTGCCAATATTTCCGCTCATTTTCATGGAAGATACCTTCTG 700  
K R N T K K V Q K N G V K V R F L G E D E L P I F R S F M E D T S E  
AAACAAAGGATTTTGACGATAGATGACGATTTTATTAATAATAGTTAAGTATTAATAAGATCGTGTGCTTGTCCCATTTAGCTTATATGATTTTGA 800  
T K D F D D R D D F Y Y N R L R Y Y K D R V L V P L A Y M D F D  
TGAATATAACAGAAATTAAGGCTGAACGCGAAGTATTAAGTAAAGATATAAATAAAGCAGTTAAGGATATAGAAAAAAGACCAGAAAAATAAAAAAGCG 900  
E Y I T E L K A E R E V L S K D I N K A V K D I E K R P E N K K A  
TATAATAAAGAAAATTTAGAACAACTGATTGCAACCAACCAAAAAATAGATGAAGCCACTGCTTACAGAGAAGCATGGTAACGAATTACC GA 1000  
Y N K K E N L E Q Q L I A N Q Q K I D E A T A L Q E K H G N E L P I  
TTTCTGCAGCTTACTTATTATTAATCCTTATGAAGTCGTTTACTATGCAGGTGGTACATCTAATGAATTTAGACATTTTGTGGTAGTTATGCAATACA 1100  
S A A Y F I I N P Y E V V Y Y A G G T S N E F R H F A G S Y A I Q  
ATGGAAGATGATTAAATATGCTATAGATCAATAATAGATAGATATAAATTTTATGGTATGATGTTTACTGAAGATGAGAAAGATGAGGTTGTT 1200  
W K M I N Y A I D H N I D R Y N F Y G I S G H F T E D A E D A G V  
GTTAAATTTAAAAAGGTTTTTAATGCAGATGTAGTATATGTTGGTGATTTTATTAACCGATTATAAGCCAAATGTACAAAATTTATACGACATTGA 1300  
V K F K K G F N A D V V E Y V G D F I K P I N K P M Y K I Y T T L K  
AAAAATTAAGGATATAAAGAAATAAacataaataagaagggaactaagctagaatgaaatttacagagtta 1371  
K I K D K K K ///

FIG.13